Applicants: Hong Chen
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 USES THEREOF
Attorney/Agent: Kerri Pollard Schray
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AATTCGCCCT TCAGCTCCAA TTGCTCTATG TTTAGAATTG CCTCTTTTTC AAGATGGATT  60
TCCTTCACAG GAATGGGAGTG CTCATAAATTC AGCATTTGCA GAAGGACTAC CGAGCTTACT 120
ACACTTTCT AAATTTTATG TCCAATGTTG GAGACCCCAG GAATATCTTT TTCATTTATT 180
TTCCACTTTG TTTTCAATTT AATCAGACAG TTGGAACCAA GATGATATGG GTAGCAGTCA 240
TTGGGATTG GTTAAATCTT ATATTTAAAT GGATATATTT TGGTCATCGA CCTTACTGGT 300
GGGTCCAAGA AACTCAGATT TACCCAAATC ACTCAAGTCC ATGCCTTGAA CAGTTCCCTA 360
CTACATGTGA AACAGGTCCA GGAAGTCCAT CTGGCCATGC AATGGGCGCA TCCTGTGTCT 420
GGTATGTCAT GGTAACCGCT GCCCTGAGCC ACACTGTCTG TGGGATGGAT AAGTTCTCTA 480
TCACTCTGCA CAGACTGACC TGGTCATTTC TTTTGGAGTGT TTTTGGTTG ATTCAAATCA 540
GTGTCTGCAT CTCCAGAGTA TTCATAGCAA CACATTTTCC TCATCAAGTT ATTCTTGGAG 600
TAATTGGTGG CATGCTGGTG GCAGAGGCCT TTGAACACAC TCCAGGCATC CAAACGGCCA 660
GTCTGGGCAC ATACCTGGAG ACCAACCTCT TTCTCTTCCT GTTTGCAGTT GGCTTTTACC 720
TGCTTCTTAG GGTGCTCAAC ATTGACCTGC TGTGGTCCGT GCCCATAGCC AAAAAGTGGT 780
GTGCTAAACCC CGACTGGATC CACATTGACA CCACGCCTTT TGCTGGACTC GTGAGAAACC 840
TTGGGGTCCT CTTTGGCTTG GGCTTTGCAA TCAACTCAGA GATGTTCCTC CTGAGCTGCC 900
GAGGGGGAAA TAACTACACA CTGTGCTTCC GGTTGCTCTG TCATTGACAA TCATTGACAA 960
TACTCGAGCT CTACCATTTC CTCCAGATCC CGACTCACGA AGAGCATTTA TTTTATGTGC 1020
TGTCTTTTTG TAAAAGTGCA TCCATTCCCC TAACTGTGGT TGCTTTCATT CCCTACTCTG 1080
TTCATATGTT AATGAAACAA AGCGGGAAAGA AGAGTCAGTA GAAAAAAAAA                1138
```

Fig. 1

```
Met Asp Phe Leu His Arg Asn Gly Val Leu Ile Ile Gln His Leu Gln
 1               5               10              15

Lys Asp Tyr Arg Ala Tyr Tyr Thr Phe Leu Asn Phe Met Ser Asn Val
            20              25              30

Gly Asp Pro Arg Asn Ile Phe Phe Ile Tyr Phe Pro Leu Cys Phe Gln
        35              40              45

Phe Asn Gln Thr Val Gly Thr Lys Met Ile Trp Val Ala Val Ile Gly
    50              55              60

Asp Trp Leu Asn Leu Ile Phe Lys Trp Ile Leu Phe Gly His Arg Pro
65              70              75              80

Tyr Trp Trp Val Gln Glu Thr Gln Ile Tyr Pro Asn His Ser Ser Pro
            85              90              95

Cys Leu Glu Gln Phe Pro Thr Thr Cys Glu Thr Gly Pro Gly Ser Pro
        100             105             110

Ser Gly His Ala Met Gly Ala Ser Cys Val Trp Tyr Val Met Val Thr
            115             120             125

Ala Ala Leu Ser His Thr Val Cys Gly Met Asp Lys Phe Ser Ile Thr
        130             135             140
```

Fig. 2A

```
Leu His Arg Leu Thr Trp Ser Phe Leu Trp Ser Val Phe Trp Leu Ile
145             150             155             160

Gln Ile Ser Val Cys Ile Ser Arg Val Phe Leu Ile Ala Thr His Phe Pro
                165             170             175

His Gln Val Ile Leu Gly Val Ile Gly Gly Met Leu Val Ala Glu Ala
                    180             185             190

Phe Glu His Thr Pro Gly Ile Gln Thr Ala Ser Leu Gly Thr Tyr Leu
                195             200             205

Lys Thr Asn Leu Phe Leu Phe Ala Val Gly Phe Tyr Leu Leu
                210             215             220

Leu Arg Val Leu Asn Ile Asp Leu Leu Trp Ser Val Pro Ile Ala Lys
            225             230             235             240

Lys Trp Cys Ala Asn Pro Asp Trp Ile His Ile Asp Thr Thr Pro Phe
                245             250             255

Ala Gly Leu Val Arg Asn Leu Gly Val Leu Phe Gly Leu Gly Phe Ala
                260             265             270

Ile Asn Ser Glu Met Phe Leu Leu Ser Cys Arg Gly Gly Asn Asn Tyr
                275             280             285
```

Fig. 2B

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Thr Leu Ser Phe Arg Leu Leu Cys Ala Leu Thr Ser Leu Thr Ile Leu
290   295   300

Gln Leu Tyr His Phe Leu Gln Ile Pro Thr His Glu Glu His Leu Phe
305   310   315   320

Tyr Val Leu Ser Phe Cys Lys Ser Ala Ser Ile Pro Leu Thr Val Val
325   330   335

Ala Phe Ile Pro Tyr Ser Val His Met Leu Met Lys Gln Ser Gly Lys
340   345   350

Lys Ser Gln
355

Fig. 2C

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H    1  MDFLHRNGVLIIQHLQKDYRAYYTFLNFMSNVGDPRNIFFIYFPLCFQFN
           ||||| |||| |·|||   · | ||    ||||||||||||||  || ·  |
M    1  MDFLHRSGVLIIHHLQEDYRTYYGFLNFMSNVGDPRNIFSIYFPLWFQLN

H   51  QTVGTKMIWVAVIGDWLNLIFKWILFGHRPYWWVQETQIYPNHSSPCLEQ
           ·  ||||||||||||||| |||||||||||||||· |||·|||||||||||
M   51  QNVGTKMIWVAVIGDWFNLIFKWILFGHRPYWWIQETEIYPNHSSPCLEQ

H  101  FPTTCETGPGSPSGHAMGASCVWYVMVTAALSHTVCGMDKFSITLHRLTW
           ||||||||||||||||||·|| |||||||||||    |·  ·||||||||
M  101  FPTTCETGPGSPSGHAMGSSCVWYVMVTAALSYTISRMEESSVTLHRLTW

H  151  SFLWSVFWLIQISVCISRVFIATHFPHQVILGVIGGMLVAEAFEHTPGIQ
           ||||||||||||||||||||||||||||||||||||||||||||||||·
M  151  SFLWSVFWLIQISVCISRVFIATHFPHQVILGVIGGMLVAEAFEHTPGVH

H  201  TASLGTYLKTNLFLFLFAVGFYLLLRVLNIDLLWSVPIAKKWCANPDWIH
           ||  |·|·||·|·||||||·||||| |·||·|||||||||||||||||||
M  201  MASLSVYLKTNVFLFLFALGFYLLLRLFGIDLLWSVPIAKKWCANPDWIH

H  251  IDTTPFAGLVRNLGVLFGLGFAINSEMFLLSCRGGNNYTLSFRLLCALTS
           ||·|||||||||||||||||||||||||·|·||   |·|||||||||||
M  251  IDSTPFAGLVRNLGVLFGLGFAINSEMFLRSCQGENGTKPSFRLLCALTS
```

Fig. 3A

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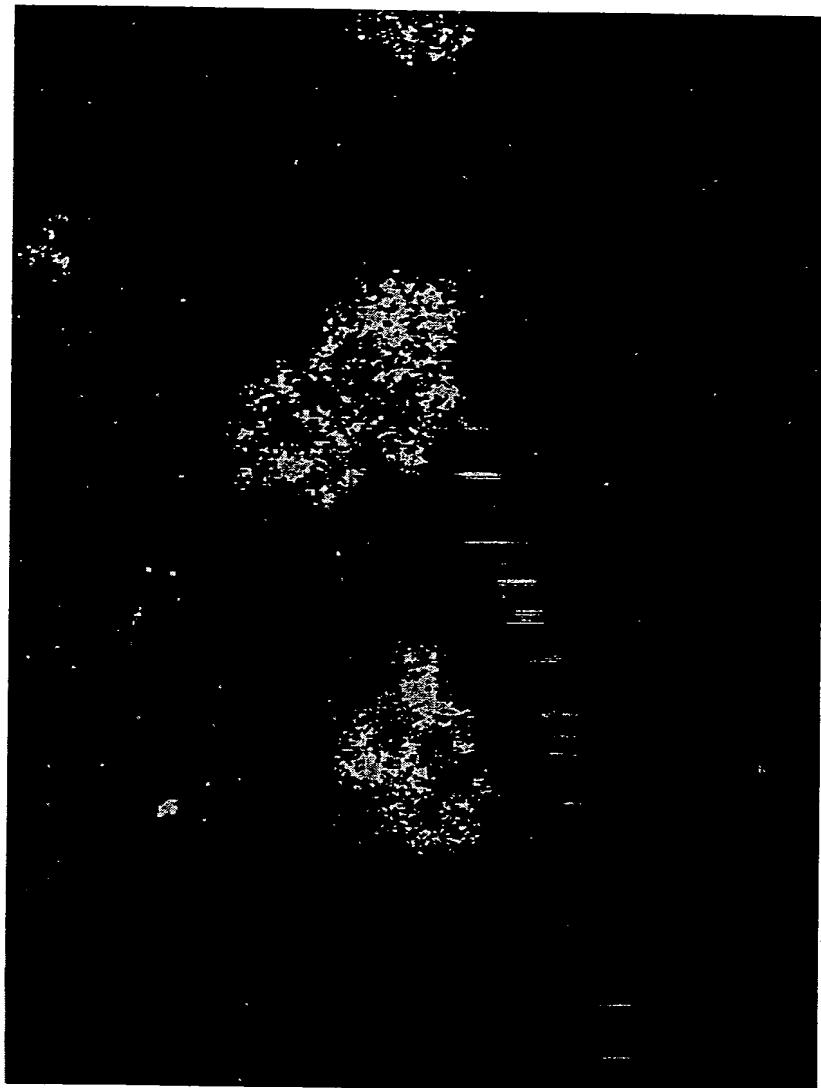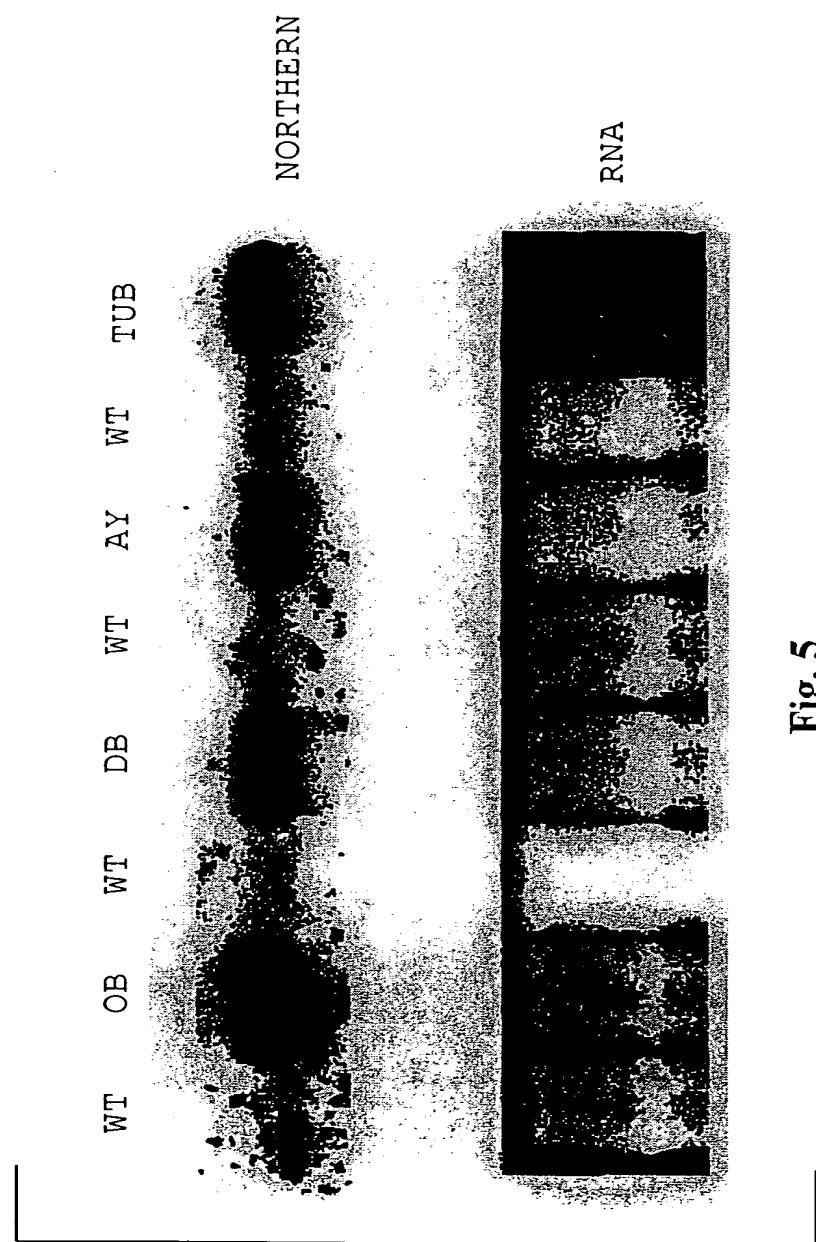　　　　　　　　Sheet 6 of 11

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```
H 301 LTILQLYHFLQIPTHEEHLFYVLSFCKSASIPLTVVAFIPYSVHMLMKQS
          : :.. | : . | :. |    : :
M 301 LTTMQLYRFIKIPTHAEPLFYLLSFCKSASIPLMVVALIPYCVHMLMRPG

H 351 GKKSQ
      || ..
M 351 DKKTK
```

Fig. 3B

Fig. 4

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Fig. 5

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Hp   MDFLHRNGVLIIQHLQKDYRAYYTFLNFMSNVGDPRNIFFIYFPLCFQFN
Mp   MDFLHRSGVLIIHHLQEDYRTYYGFLNFMSNVGDPRNIFSIYFPLWFQLN
Fl   MDLLHSWGVELAVYLQTRYGKYEGLFDLASTVADLHTTFFWLFPIWFHLR
Ml   MEEGMNILHDFGIQSTRYLQVNYQDSQDWFILVSVIADLRNAFYVLFPIWFHLK
Cl   MEKGMDVLHDFGIQSTHYLQVNYQDSQDWFILVSVIADLRNAFYVLFPIWFHLR
Hl   MEEGMNVLHDFGIQSTHYLQVNYQDSQDWFILVSVIADLRNAFYVLFPIWFHLQ

Hp   QTVGTKMIWVAVIGDWLNLIFKWILFGHRPYWWVQETQIYPNHSSPCLEQFPTT
Mp   QNVGTKMIWVAVIGDWFNLIFKWLLFGHRPYWWIQETEIYPNHSSPCLEQFPTT
Fl   RDTALRLIWVAVIGDWLNLVLKWVLFGERPYWWVHETKFYGAGPAPSLQQFPIT
Ml   ETVGINLLWVAVVGDWFNLVFKWILFGQRPYWWVLDTDYYSNSSVPLIKQFPVT
Cl   EAVGIKLLWVAVIGDWLNLVFKWILFGQRPYWWVMDTDYYSNTSVPLIKQFPVT
Hl   EAVGIKLLWVAVIGDWLNLVFKWILFGQRPYWWVLDTDYYSNTSVPLIKQFPVT

Hp   CETGPGSPSGHAMGASCVWYVMVTAALSHTVCGMDKFSITLHRLTWSFLWSVFW
Mp   CETGPGSPSGHAMGSSCVWYVMVTAALSYTISRMEESSVTLHRLTWSFLWSVFW
Fl   CETGPGSPSGHAMGAAGVWYVMVTALLS--IAREKQCPPLLYRFLYIGLWMLMG
Ml   CETGPGSPSGHAMGAAGVYYVMVTSTLA--IFRGKKKPTYGFRCLNVILWLGFW
Cl   CETGPGSPSGHAMGTAGVYYVMVTSTLS--IFRGRKRPTYRFRCLNILLWLGFW
Hl   CETGPGSPSGHAMGTAGVYYVMVTSTLS--IFQGKIKPTYRFRCLNVILWLGFW
```

Fig. 6A

```
Hp  LIQISVCISRVFIATHFPHQVILGVIGGMLVAEAFEHTPGIQTASLGTYLKTNL
Mp  LIQISVCISRVFIATHFPHQVILGVIGGMLVAEAFEHTPGVHMASLSVYLKTNV
Fl  LVELVVCISRVYMAAHFPHQVIAGIITGTLVAEVVSKEKWIYSASLKKYFLITL
Ml  AVQLNVCLSRIYLAAHFPHQVVAGVLSGIAVAETFSHIRGIYNASLRKYCLITI
Cl  AVQLNVCLSRIYLAAHFPHQVVAGVLSGIAVAETFRHIQSIYNASLKKYFLITF
Hl  AVQLNVCLSRIYLAAHFPHQVVAGVLSGIAVTETFSHIHSIYNASLKKYFLITF


Hp  FLFLFAVGFYLLLRVLNIDLLWSVPIAKKWCANPDWIHIDTTPFAGLVRNLGVL
Mp  FLFLFALGFYLLLRLFGIDLLWSVPIAKKWCANPDWIHIDSTPFAGLVRNLGVL
Fl  FLTSFAVGFYVLLKALDVDLLWTMEKAQKWCIRPEWVHLDSAPFASLLRNMGSL
Ml  FLFGFALGFYLLLKGLGVDLLWTLEKAKRWCERPEWVHLDTTPFASLFKNLGTL
Cl  FLFSFAIGFYLLLKGLGVDLLWTLEKARRWCERPEWVHIDTTPFASLLKNVGTL
Hl  FLFSFAIGFYLLLKGLGVDLLWTLEKAQRWCEQPEWVHIDTTPFASLLKNLGTL


Hp  FGLGFAINSEMFLLSCRGGNNYTLSFRLLCALTSLTILQLYHFLQIPTHEEHLF
Mp  FGLGFAINSEMFLRSCQGENGTKPSFRLLCALTSLTTMQLYRFIKIPTHAEPLF
Fl  FGLGLGLHSPFYKTTKMRIMSA--PLRIGCIVISVSLLHLLDGWTFSPENHMTF
Ml  LGLGLALNSSMYRKSCKGELSKSFPFRFACIVASLVLLHLFDSLKPPSQVELIF
Cl  FGLGVTLNSSMYRESCKGKLSKWFPFFRLSCIVVSLILLHLFDSLKPPSQTELIF
Hl  FGLGLALNSSMYRESCKGKLSKWLPFFRLSSIVASLVLLHVFDSLKPPSQVELVF
```

Fig. 6B

Hp YVLSFCKSASIPLTVVAFIPYSV-HMLMKQSGKKSQ
Mp YLLSFCKSASIPLMVVALIPYCV-HMLMRPGDKKTK
F1 YALSFGKSAVALLIPTTLVPWALSKIYPVKTEGKNL
M1 YILSFCKSATVPFASVSLIPYCLARILG-QTHKKSL
C1 YTLSFCKSAAVPLASVSLIPYCLARVFD-QPDKKSL
H1 YVLSFCKSAVVPLASVSVIPYCLAQVLG-QPHKKSL

Fig. 6C